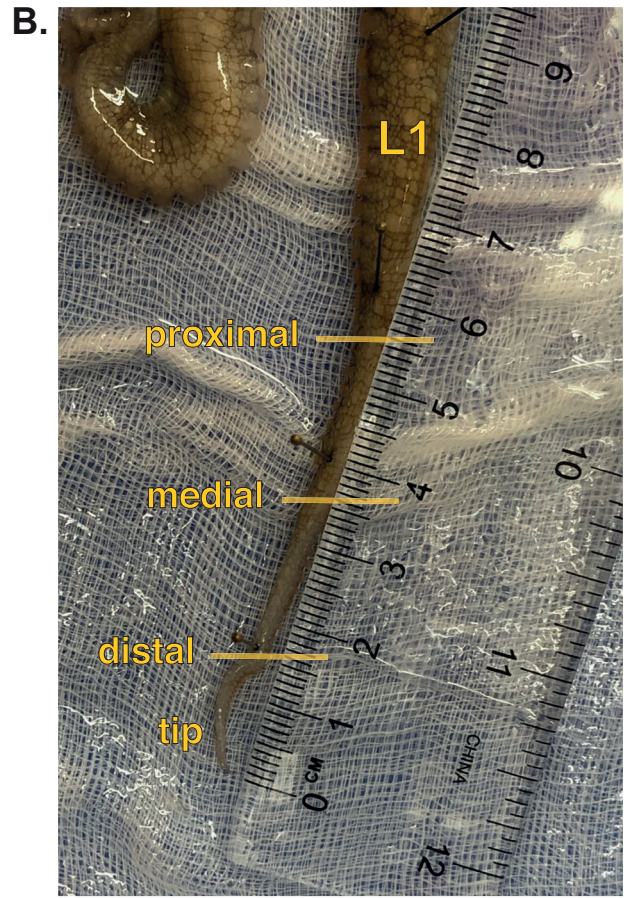
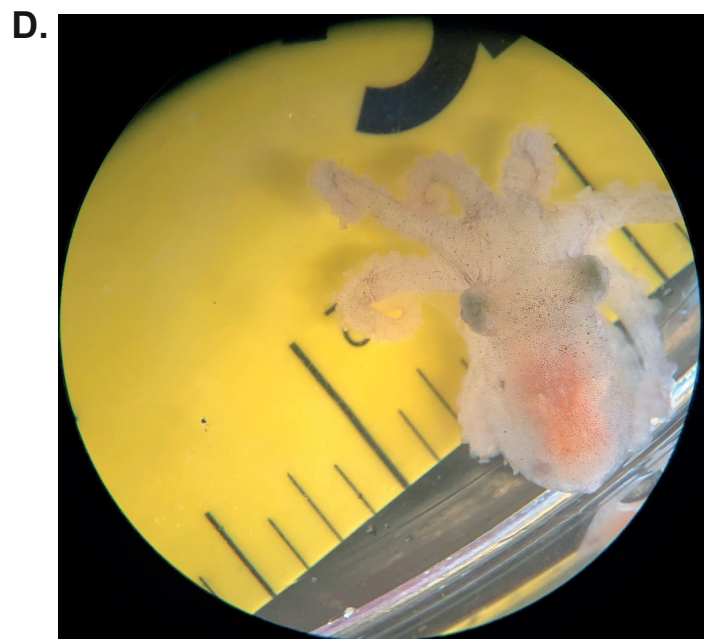
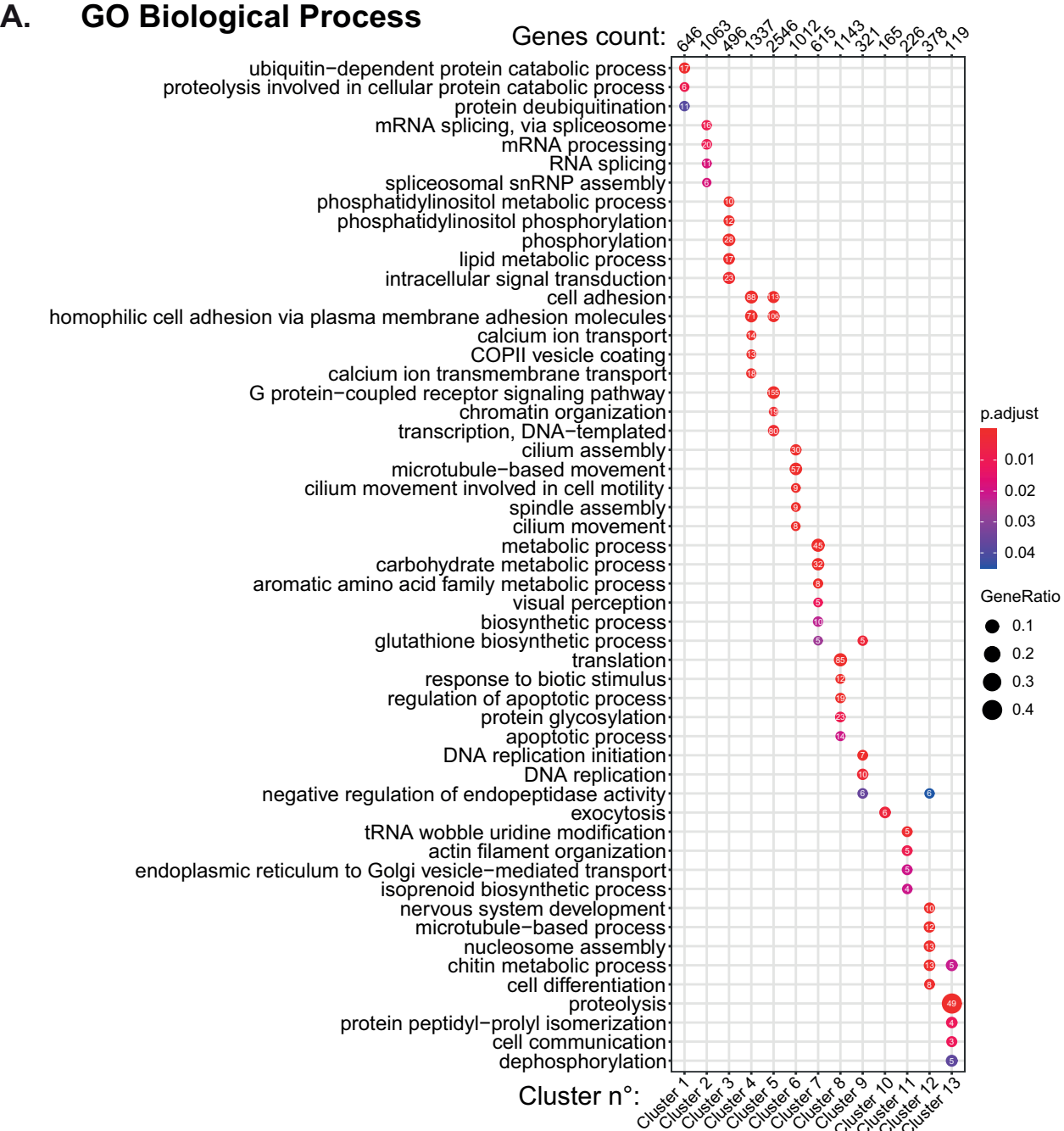


***O. bimaculoides* Adult**

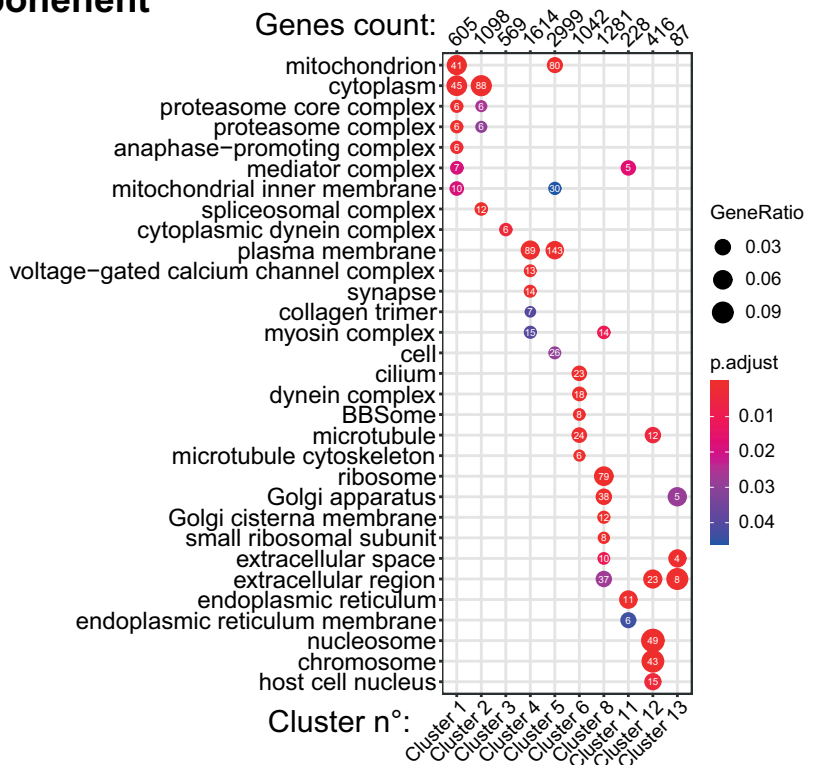


***O. bimaculoides* Hatchling 30 days**





B. GO Cellular Component



A. Metazoa 50: DNMT1



B. Metazoa 50: UHRF1



A. DNMT1_OCTBM

Domain	Pfam ID	Bit Score	Domain E-values	
			Ind.	Cond.
RFTD	DNMT1-RFD	138.86	1.2e-40	2.7e-44
CXXC	zf-CXXC	47.88	1.0e-12	2.2e-16
BAH1	BAH	55.25	5.7e-15	1.3e-18
BAH2	BAH	55.65	4.3e-15	9.5e-19
CTD (C-5 cytosine methyltransferase)	DNA_methylase	165.85	1.5e-48	3.4e-52

HMMER (*O. bimaculoides* protein sequence vs. entire protein sequence database)

C. UHRF1_OCTBM

Domain	Pfam ID	Bit Score	Domain E-values	
			Ind.	Cond.
UBL	ubiquitin	52.61	2.8e-14	6.2e-18
TTD	TTD	171.29	1.3e-50	2.9e-54
PHD	PHD	47.58	1.1e-12	2.5e-16
SRA	SAD_SRA	190.13	1.9e-56	4.2e-60
RING	Not unique ID	Manually annotated	% identity (count) = 64.1% (39)	

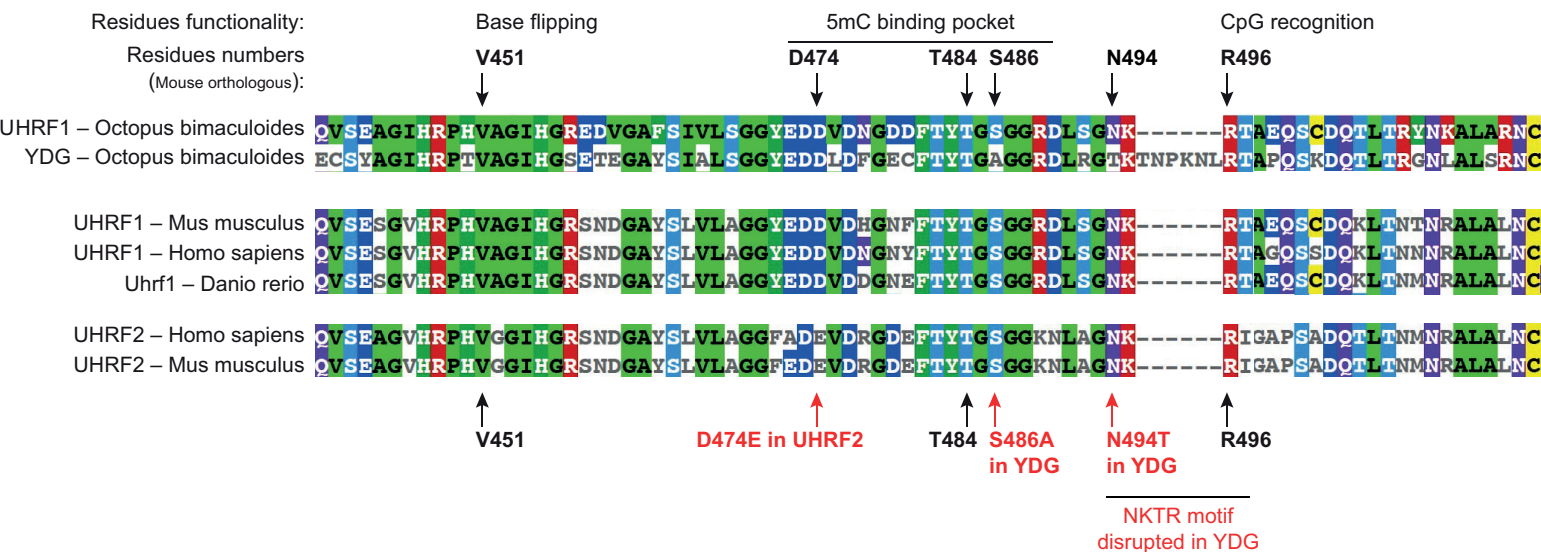
HMMER (*O. bimaculoides* protein sequence vs. entire protein sequence database)

E. YDG_OCTBM

Domain	Pfam ID	Bit Score	Domain E-values	
			Ind.	Cond.
SRA	SAD_SRA	195.46	4.3e-58	2.4e-62

HMMER (*O. bimaculoides* protein sequence vs. entire protein sequence database)

G.



B. DNMT1_OCTBM

Organism	UniProt ID	Gene ID	% of Identity
Octopus bimaculoides	A0A0L8GEZ1	<i>Ocbimv22034501m.g</i>	100.00
Danio rerio	Q8QGB8	<i>dnmt1</i>	56.01
Homo sapiens	P26358	<i>DNMT1</i>	54.79
Mus musculus	P13864	<i>Dnmt1</i>	52.24

ClustalOmega multiple protein sequence alignment

D. UHRF1_OCTBM

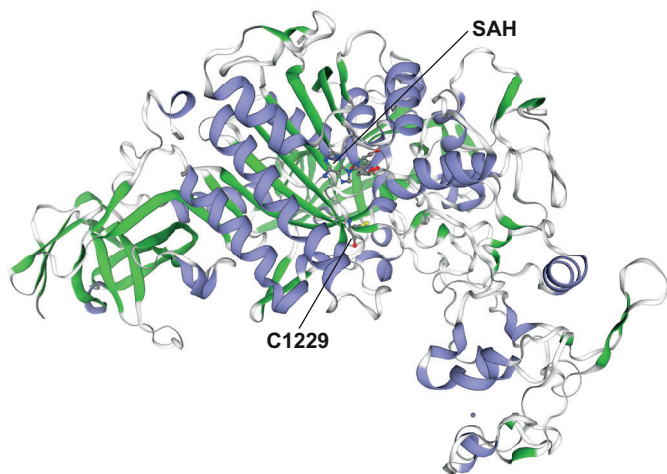
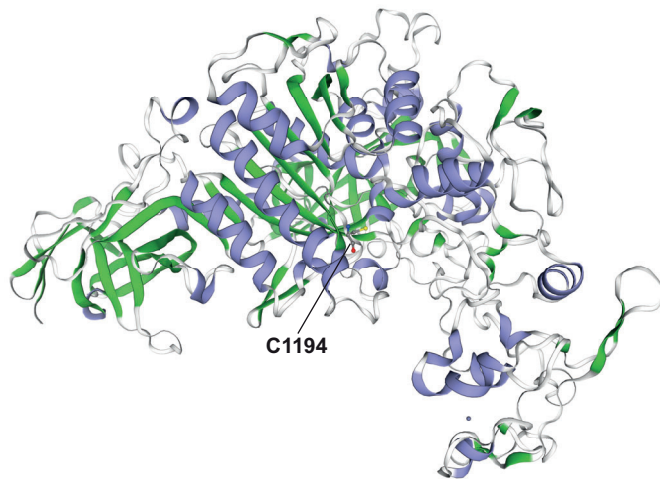
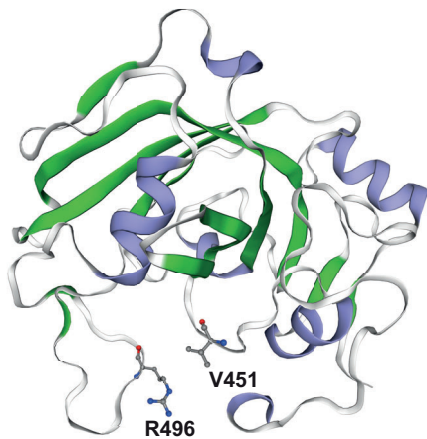
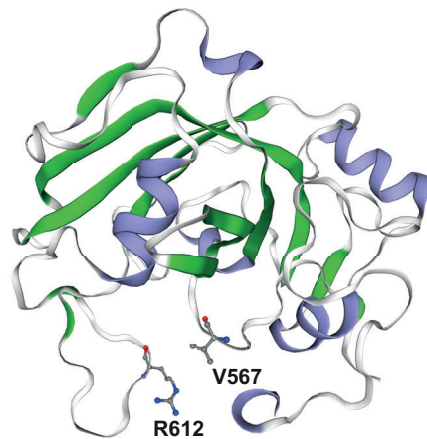
Organism	UniProt ID	Gene ID	% of Identity
Octopus bimaculoides	A0A0L8IC59	<i>Ocbimv22021185m.g</i>	100.00
Danio rerio	E7EF3	<i>uhrf1</i>	56.37
Homo sapiens	Q96T88	<i>UHRF1</i>	55.88
Mus musculus	Q8VDF2	<i>Uhrf1</i>	53.55
Homo sapiens	Q96PU4	<i>UHRF2</i>	50.19
Mus musculus	Q7TMI3	<i>Uhrf2</i>	50.00

ClustalOmega multiple protein sequence alignment

F. YDG_OCTBM

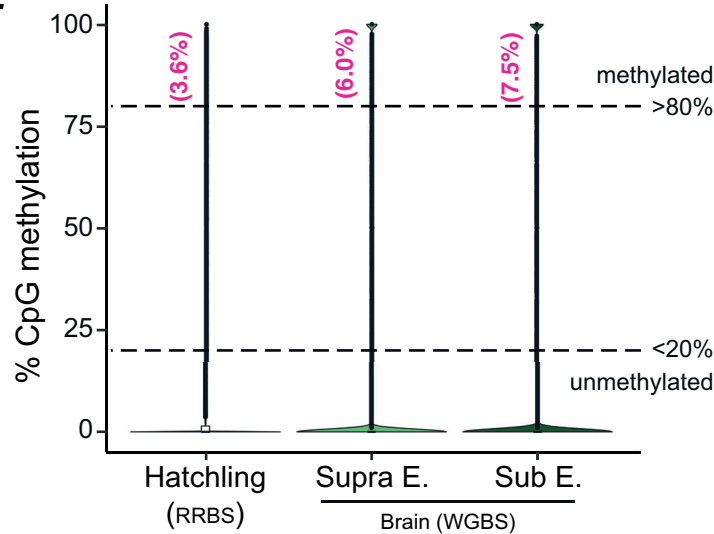
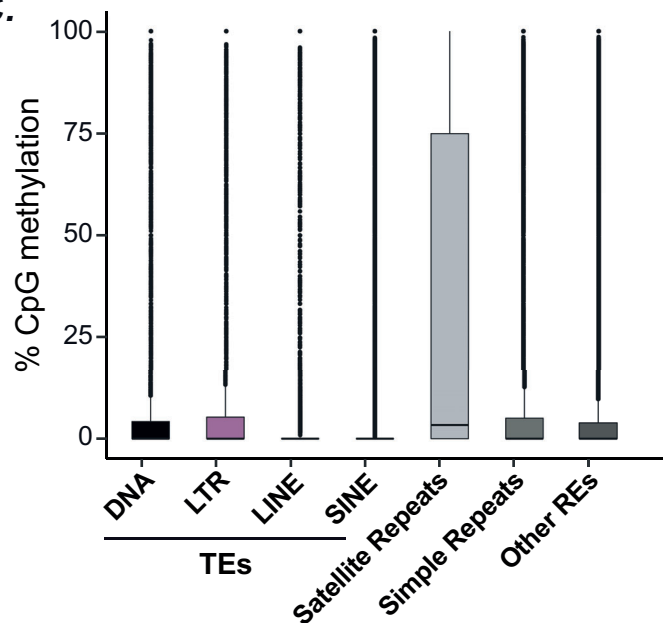
Organism	UniProt ID	Gene ID	% of Identity
Octopus bimaculoides	A0A0L8H8G0	<i>Ocbimv22020196m.g</i>	100.00
Mus musculus	Q8VDF2	<i>Uhrf1</i>	34.46
Homo sapiens	Q96T88	<i>UHRF1</i>	33.53
Danio rerio	E7EF3	<i>uhrf1</i>	32.42
Mus musculus	Q7TMI3	<i>Uhrf2</i>	31.69
Homo sapiens	Q96PU4	<i>UHRF2</i>	31.08

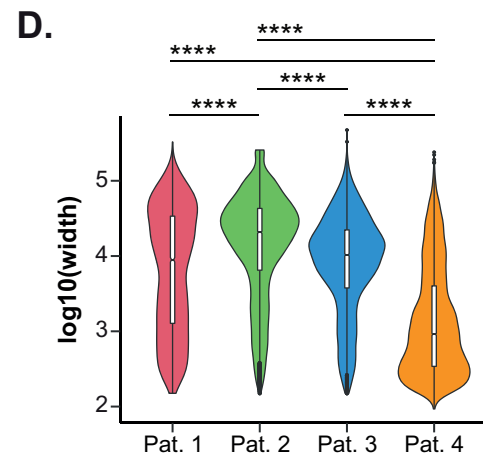
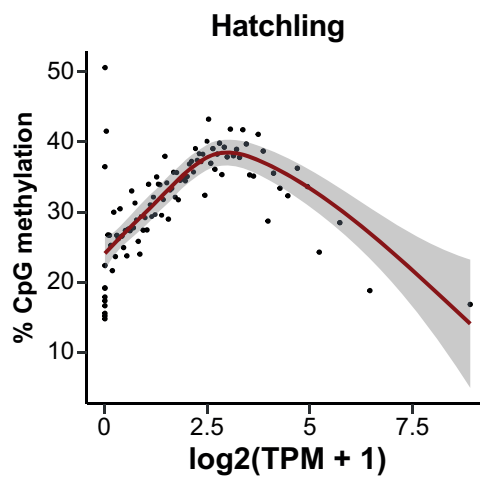
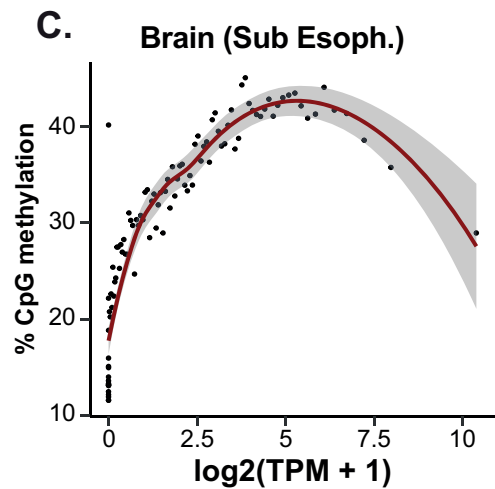
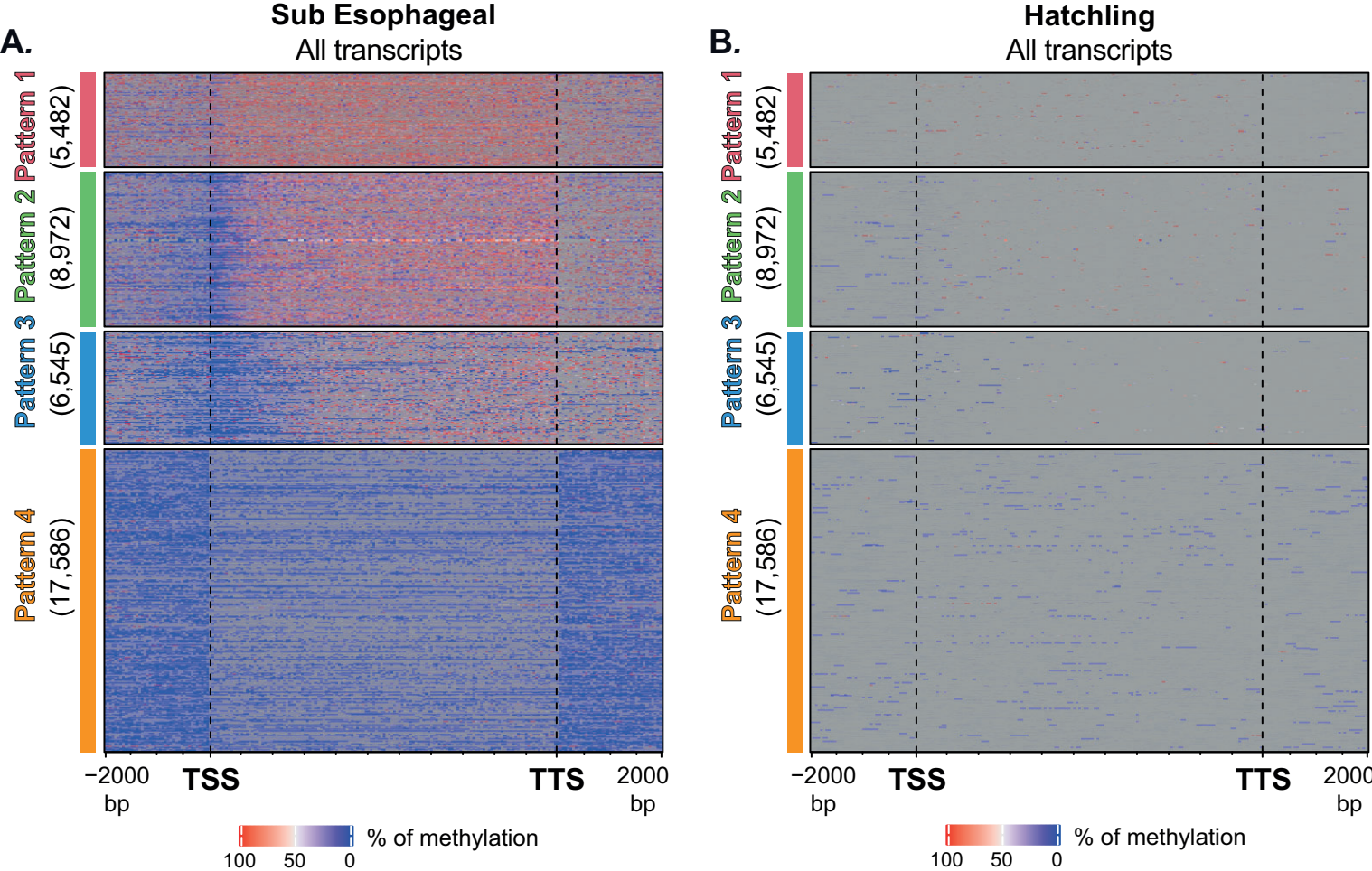
ClustalOmega multiple protein sequence alignment

A.**DNMT1**
Mouse BAH1/2 & CTD domains**B.****DNMT1**
Octopus BAH1/2 & CTD domains**C.****UHRF1**
Mouse SRA domain**D.****UHRF1**
Octopus SRA domain

A.

Total CpGs	80,660,576		
Sample	Covered CpGs	Methylated CpGs (>80%)	Unmethylated CpGs (<20%)
RRBS Hatchling	2,403,266	87,223	2,172,200
Percent of total	2.98%	3.63%	90.39%
WGBS Supra E	64,845,686	3,897,277	55,918,461
Percent of total	80.39%	6.01%	86.23%
WGBS Sub E	47,053,504	3,542,069	40,626,272
Percent of total	58.34%	7.53%	86.34%

B.**C.****REs in Hatchling**

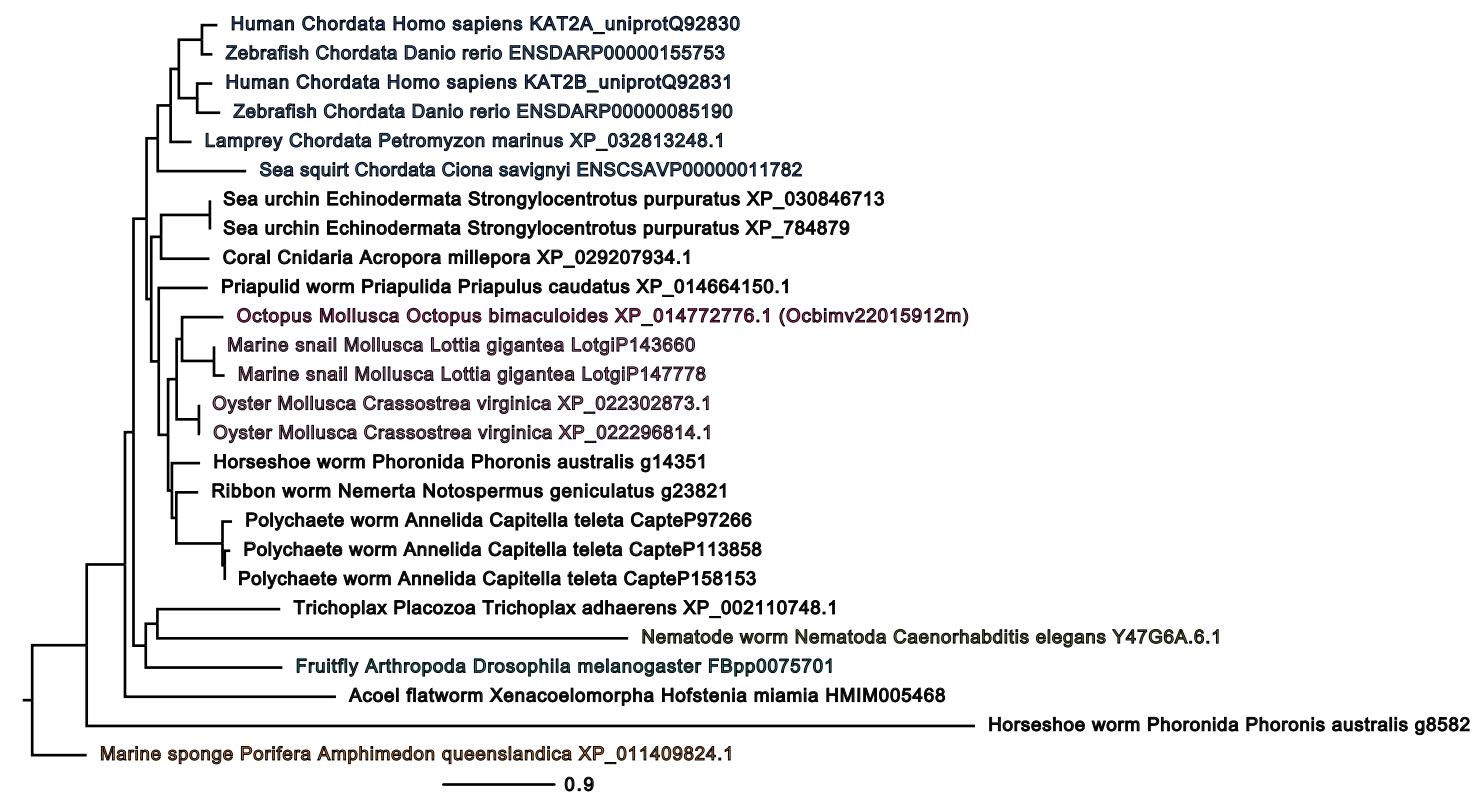


Suppl. Figure 7

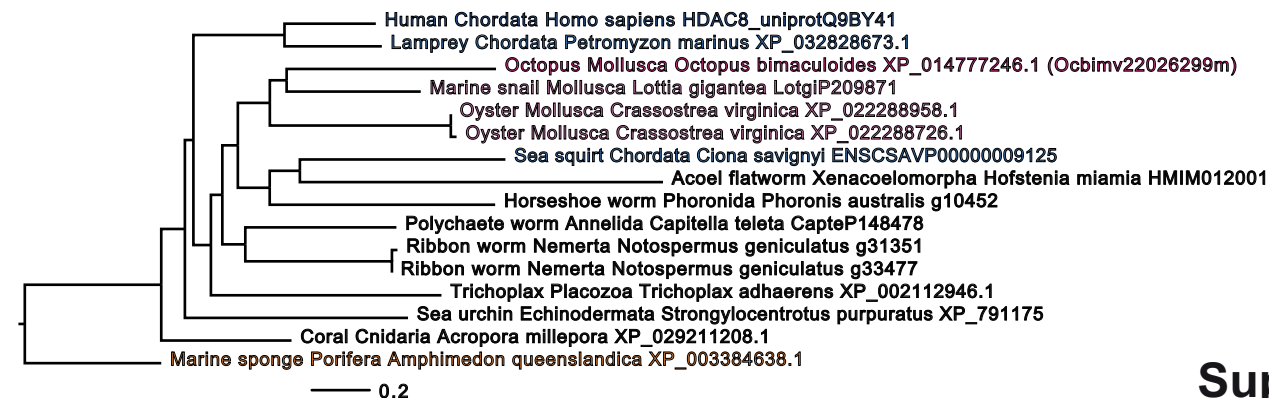
A. EZH2



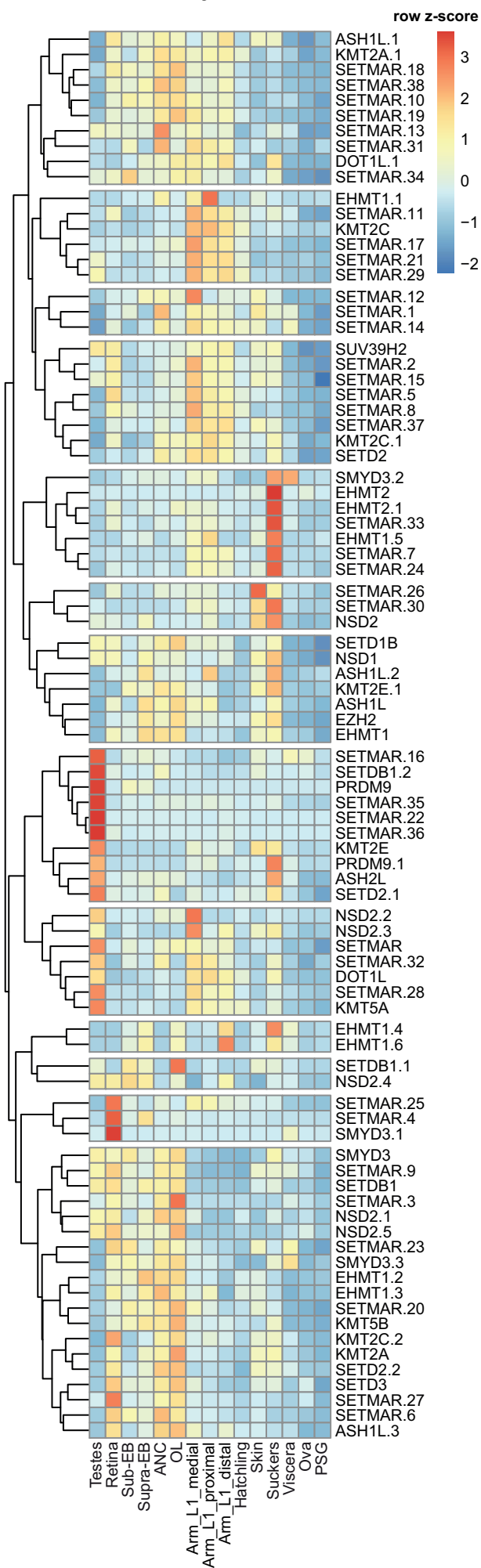
B. KAT2A



C. HDAC8



A. Histone methyl-transferases



B. Histone acetylation

